












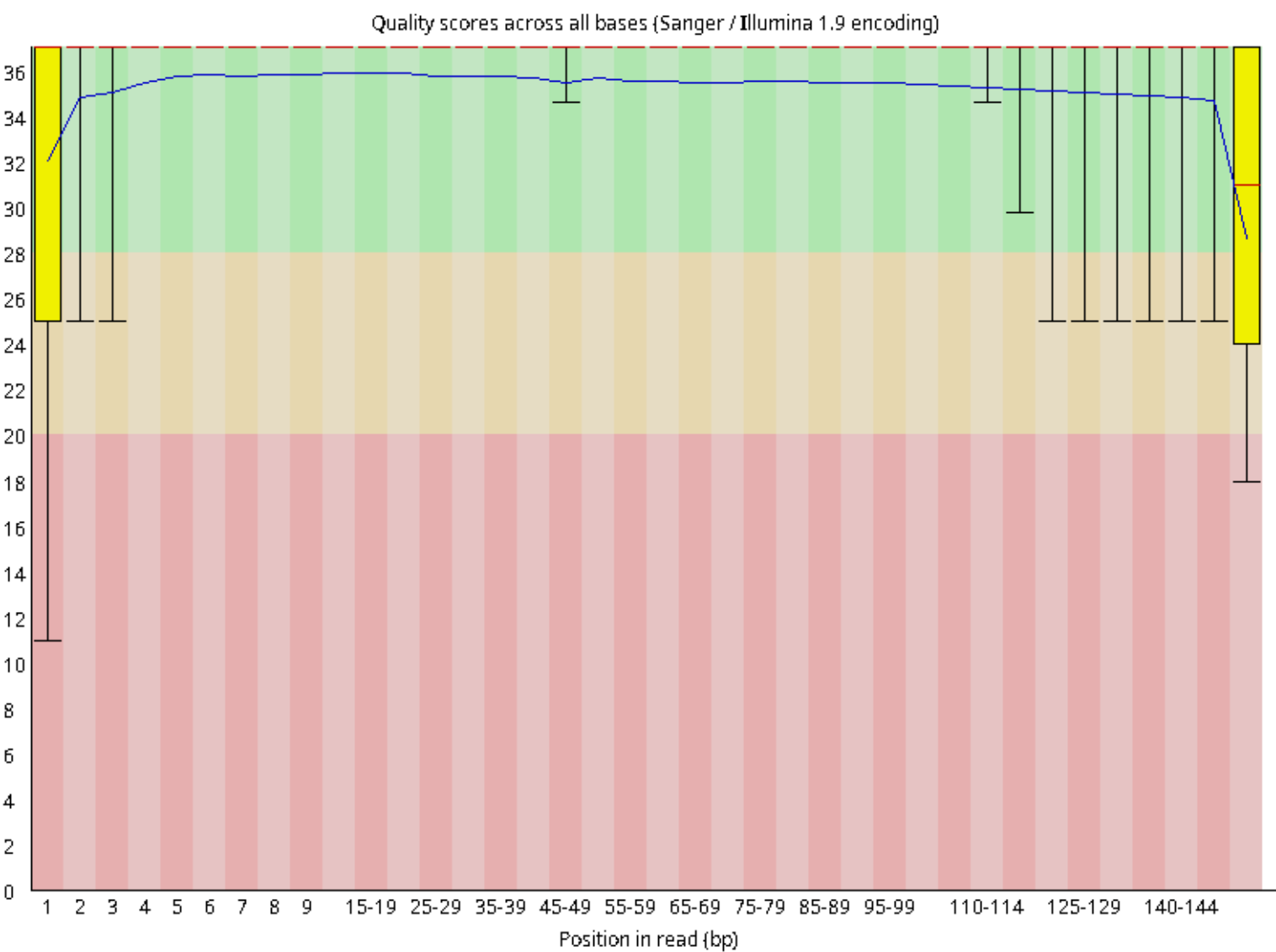
## Summary

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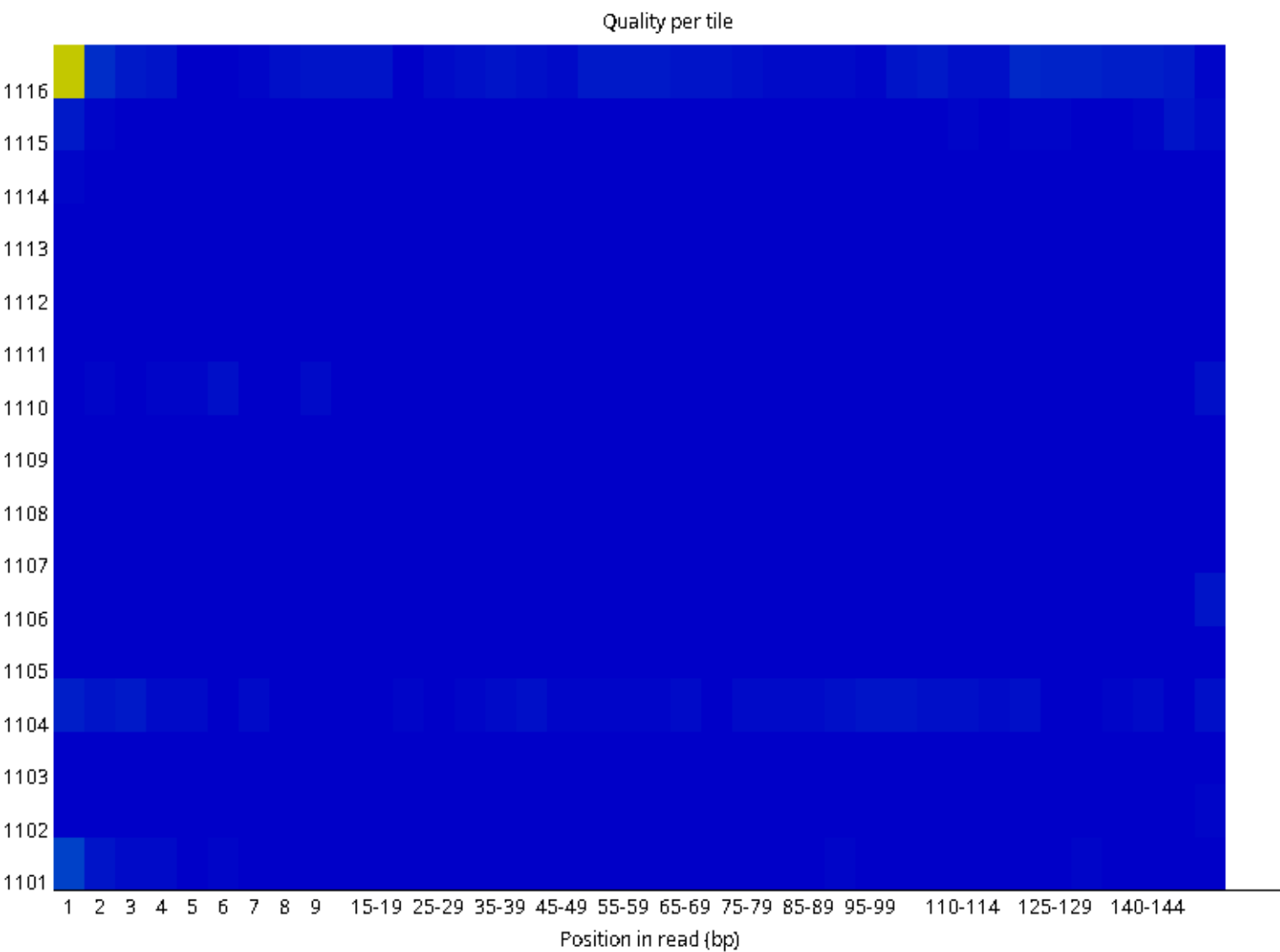
## Basic Statistics

Measure	Value
Filename	SRR33784444_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	122837
Sequences flagged as poor quality	0
Sequence length	151
%GC	47

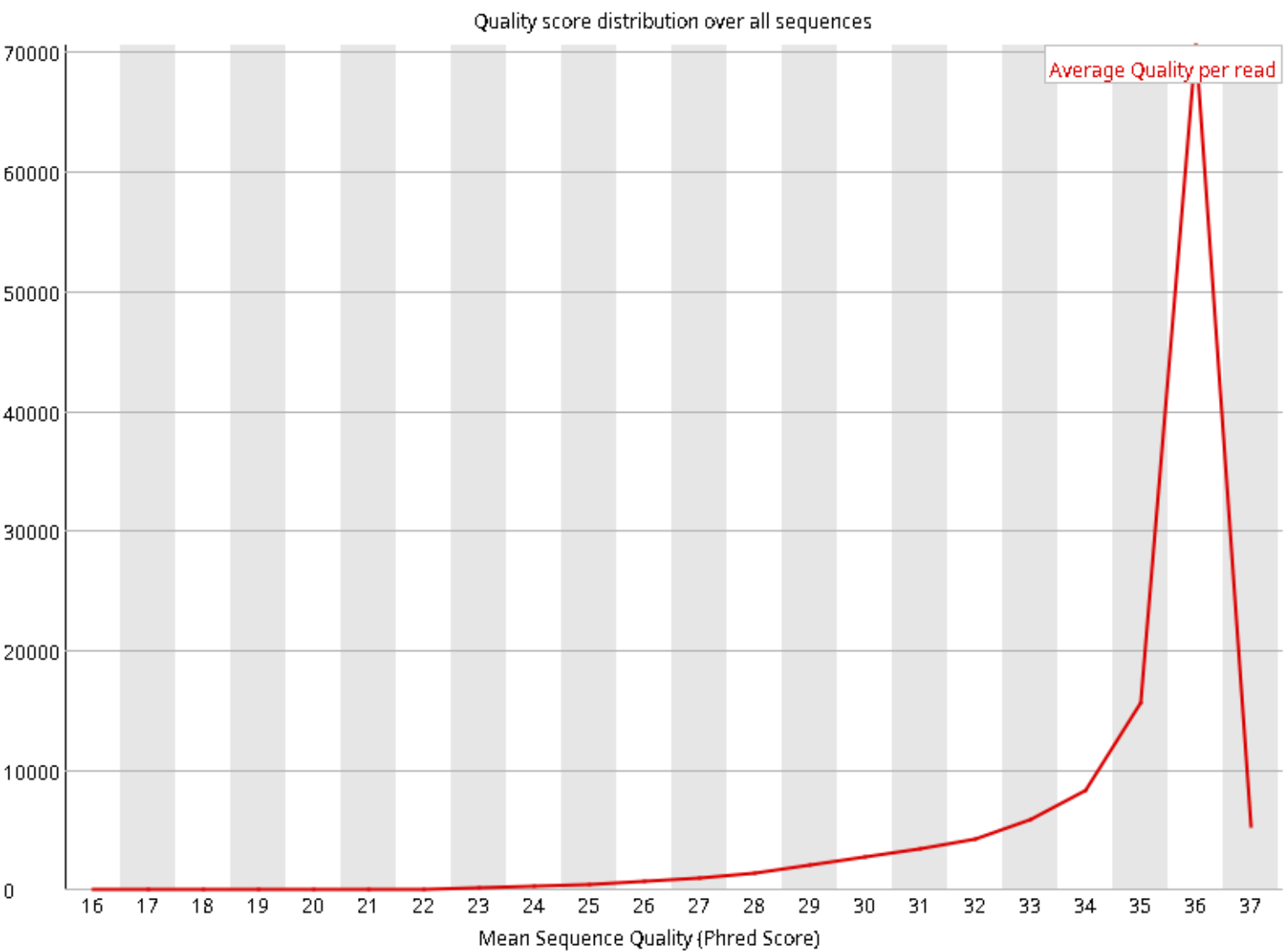
## ✔ Per base sequence quality



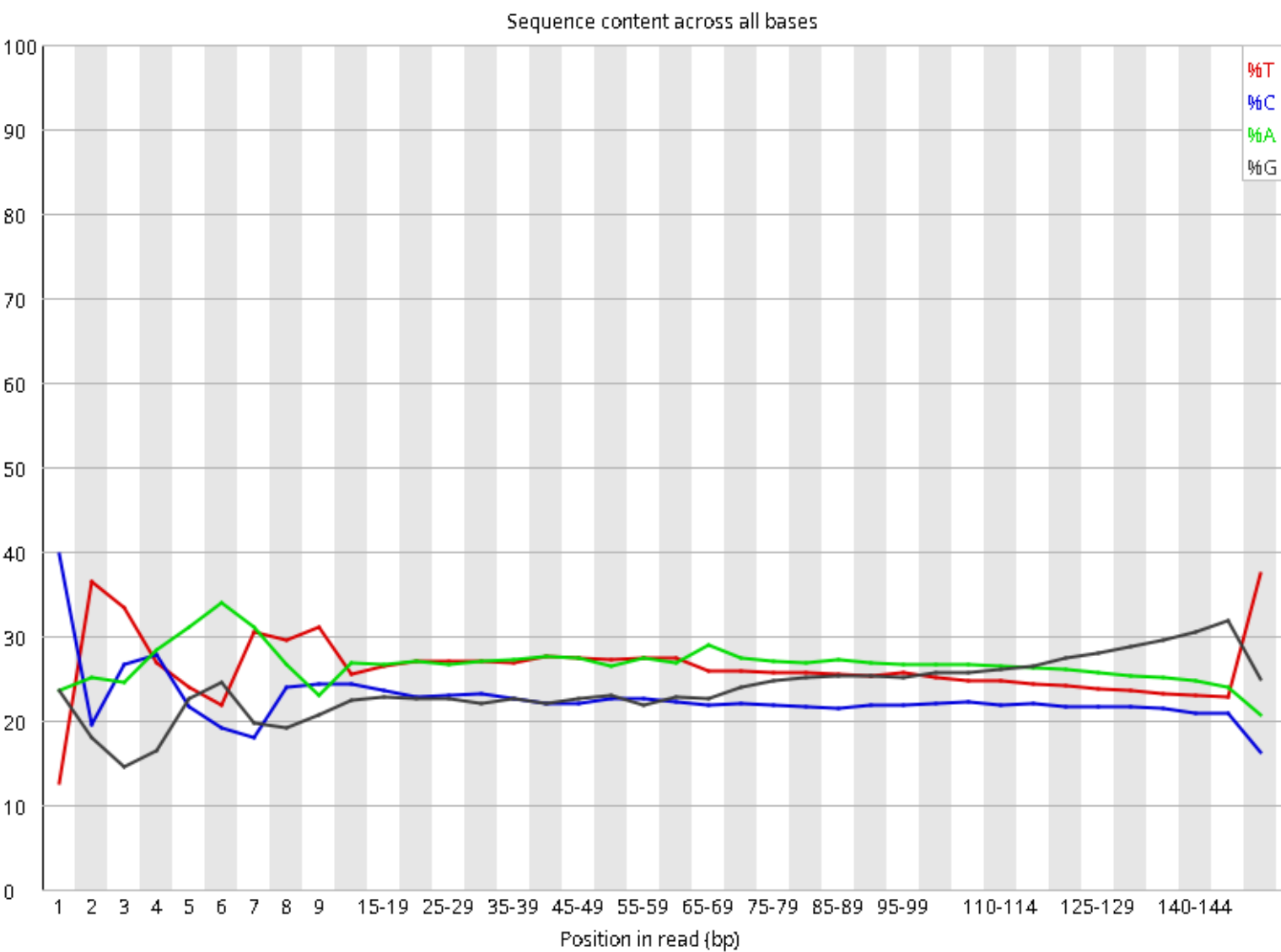
# ! Per tile sequence quality



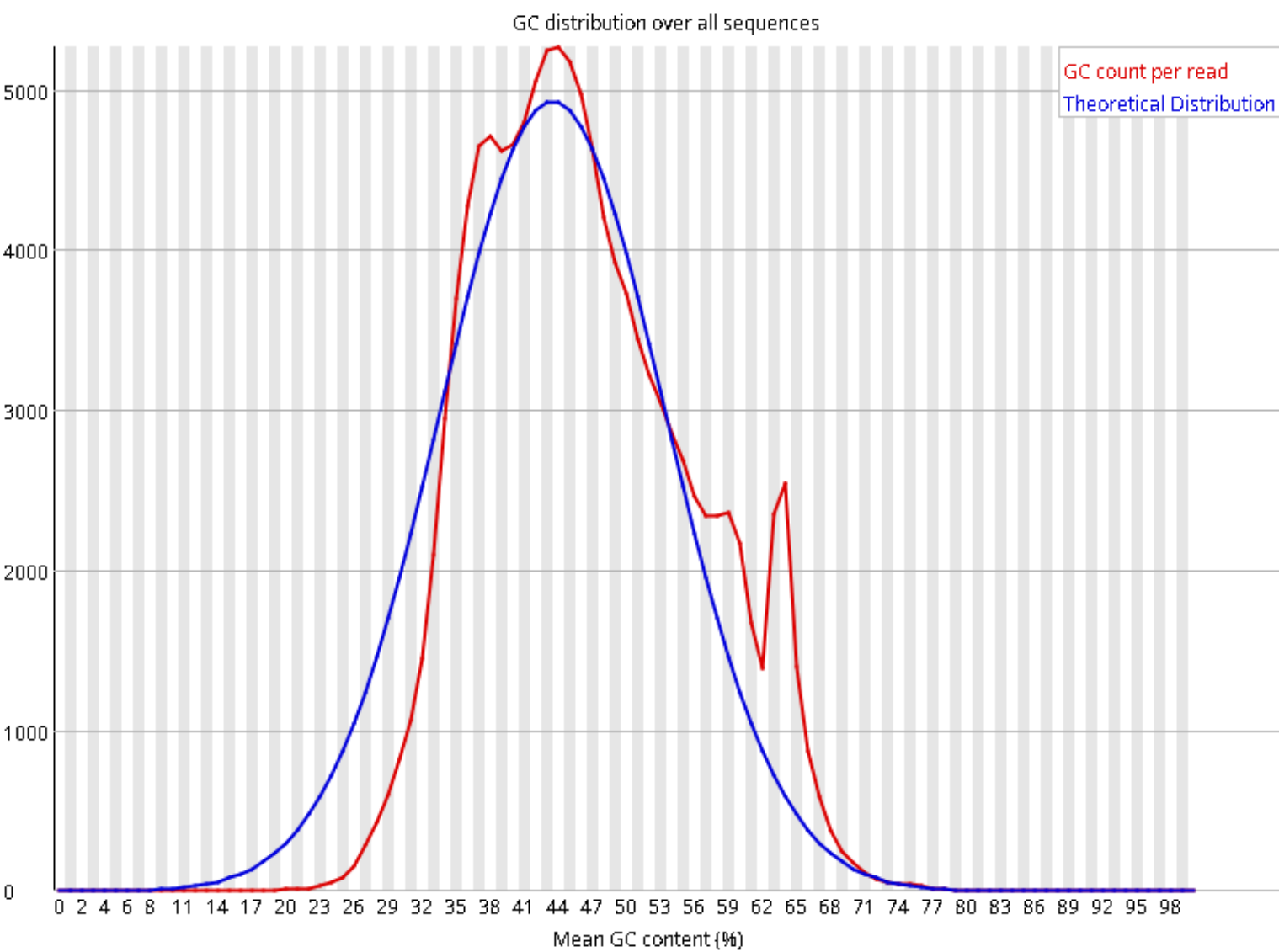
## ✔ Per sequence quality scores



## ! Per base sequence content

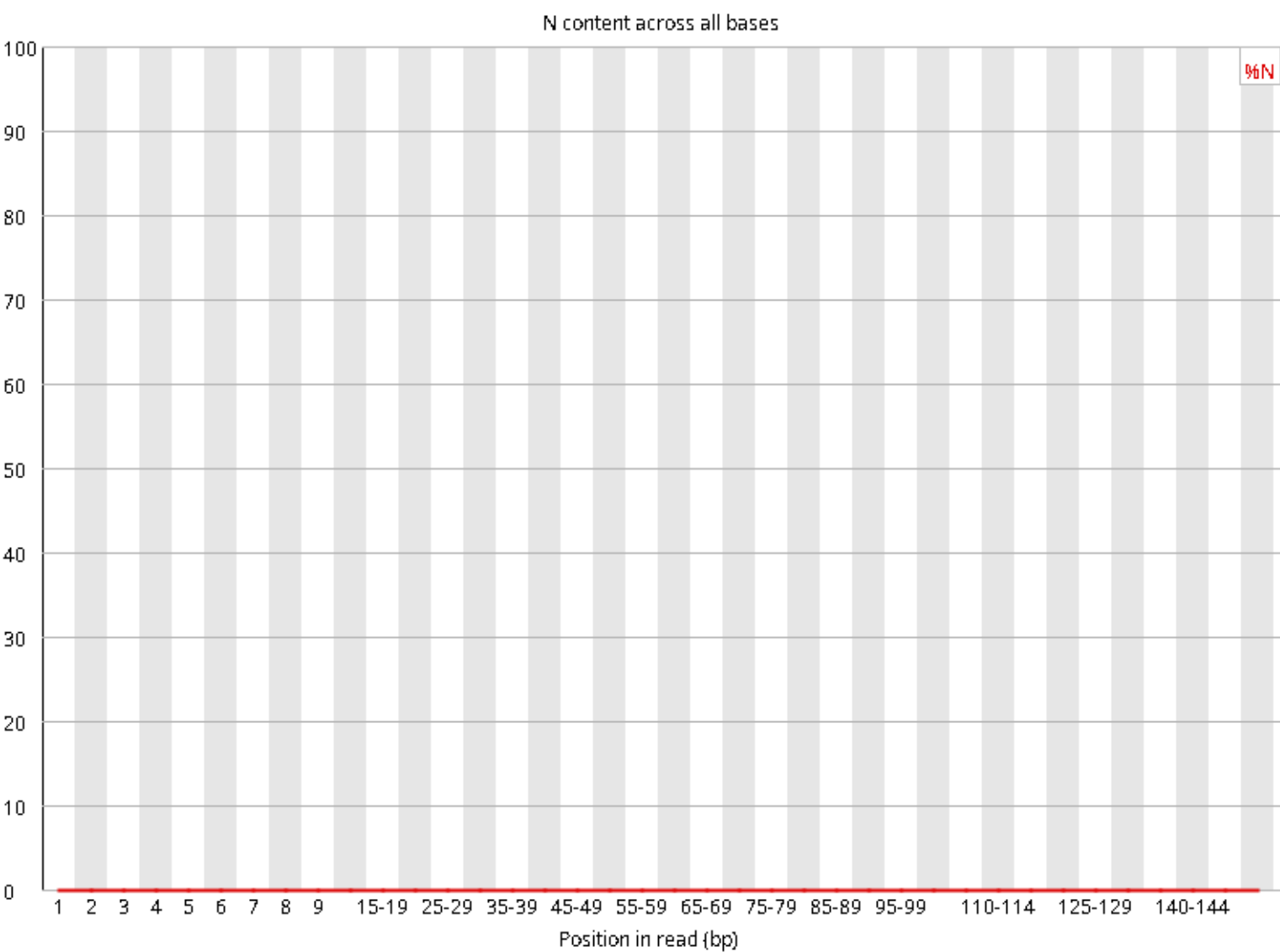


## ! Per sequence GC content

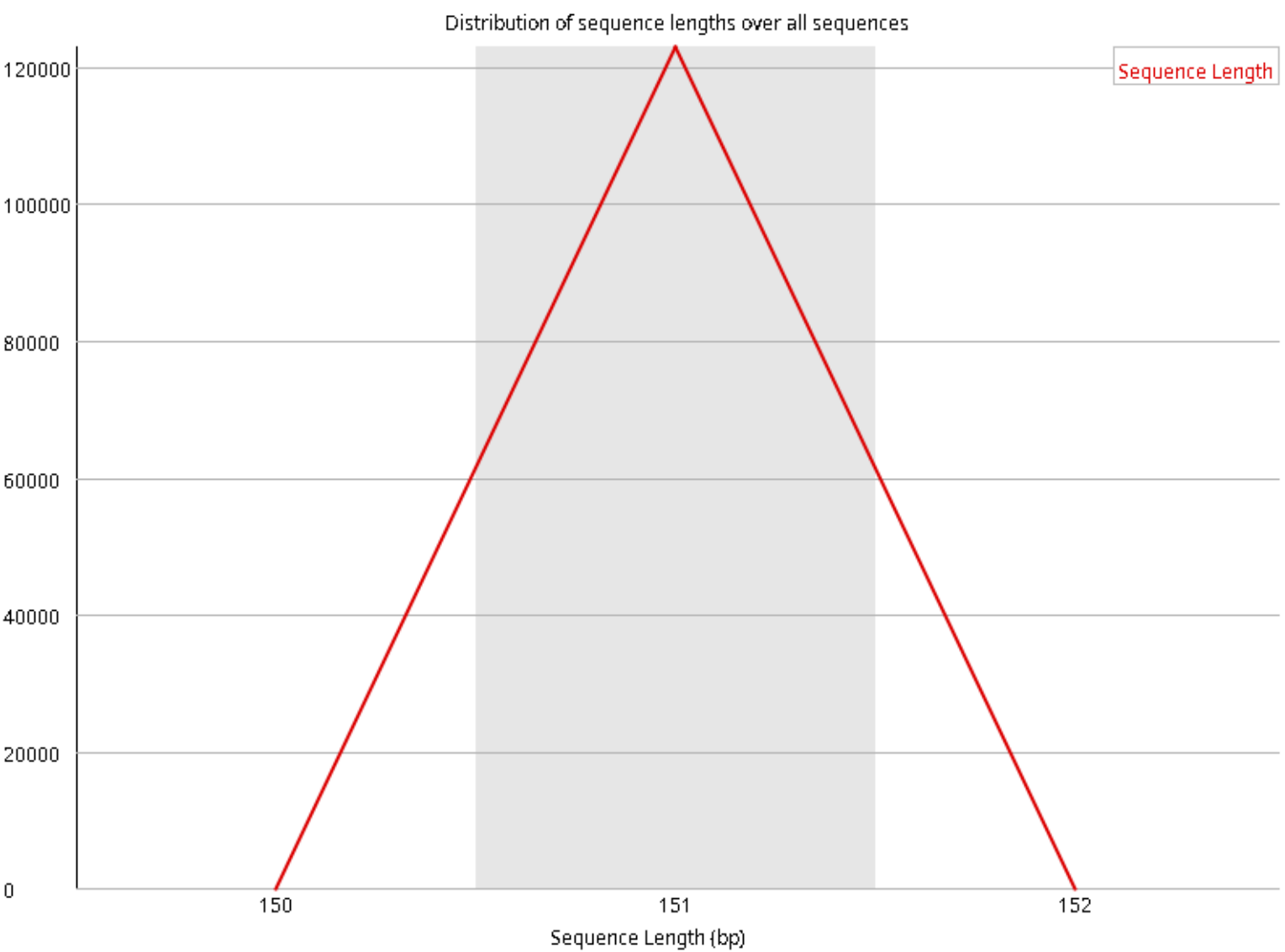




## Per base N content

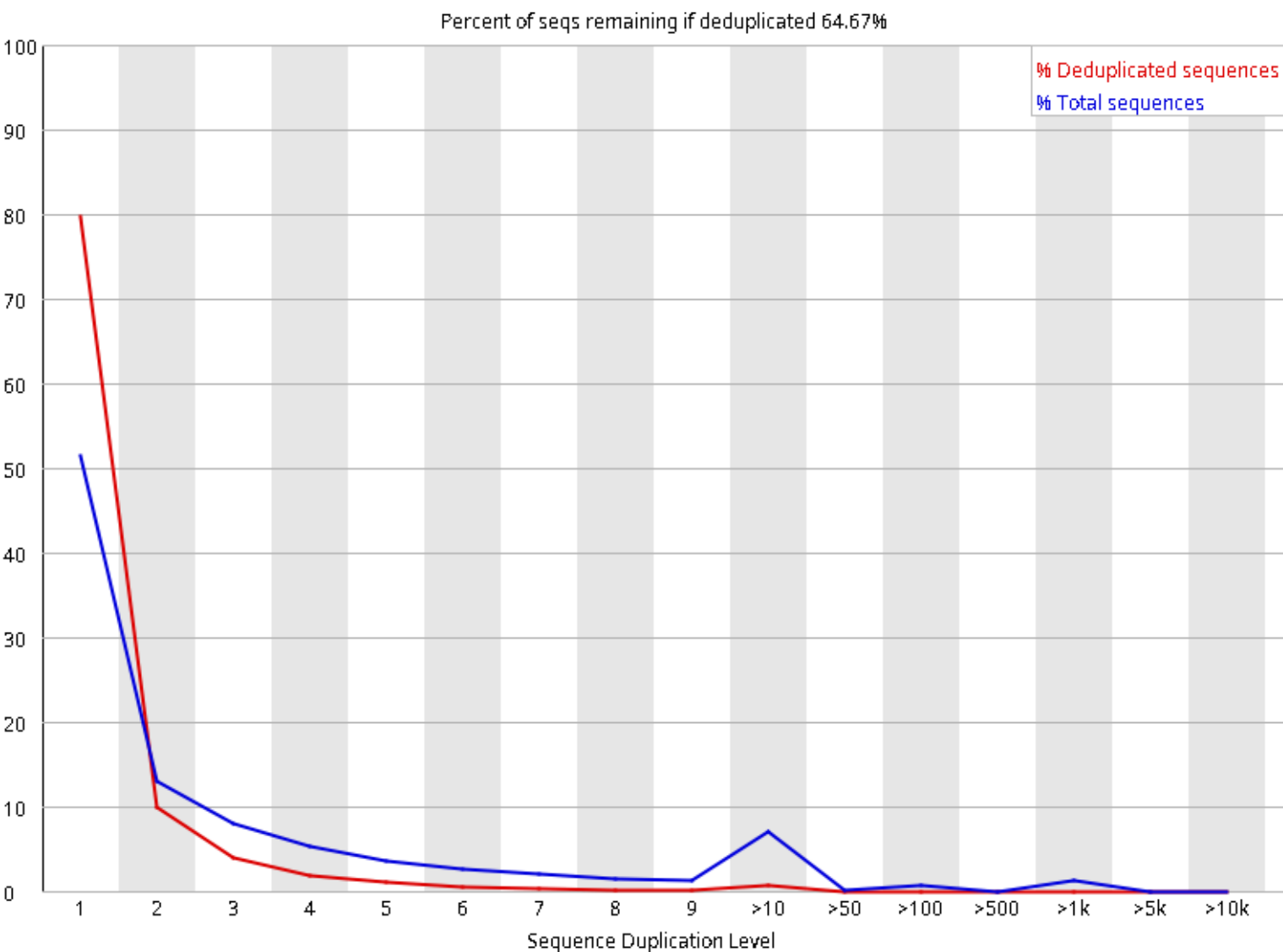


# Sequence Length Distribution





## Sequence Duplication Levels

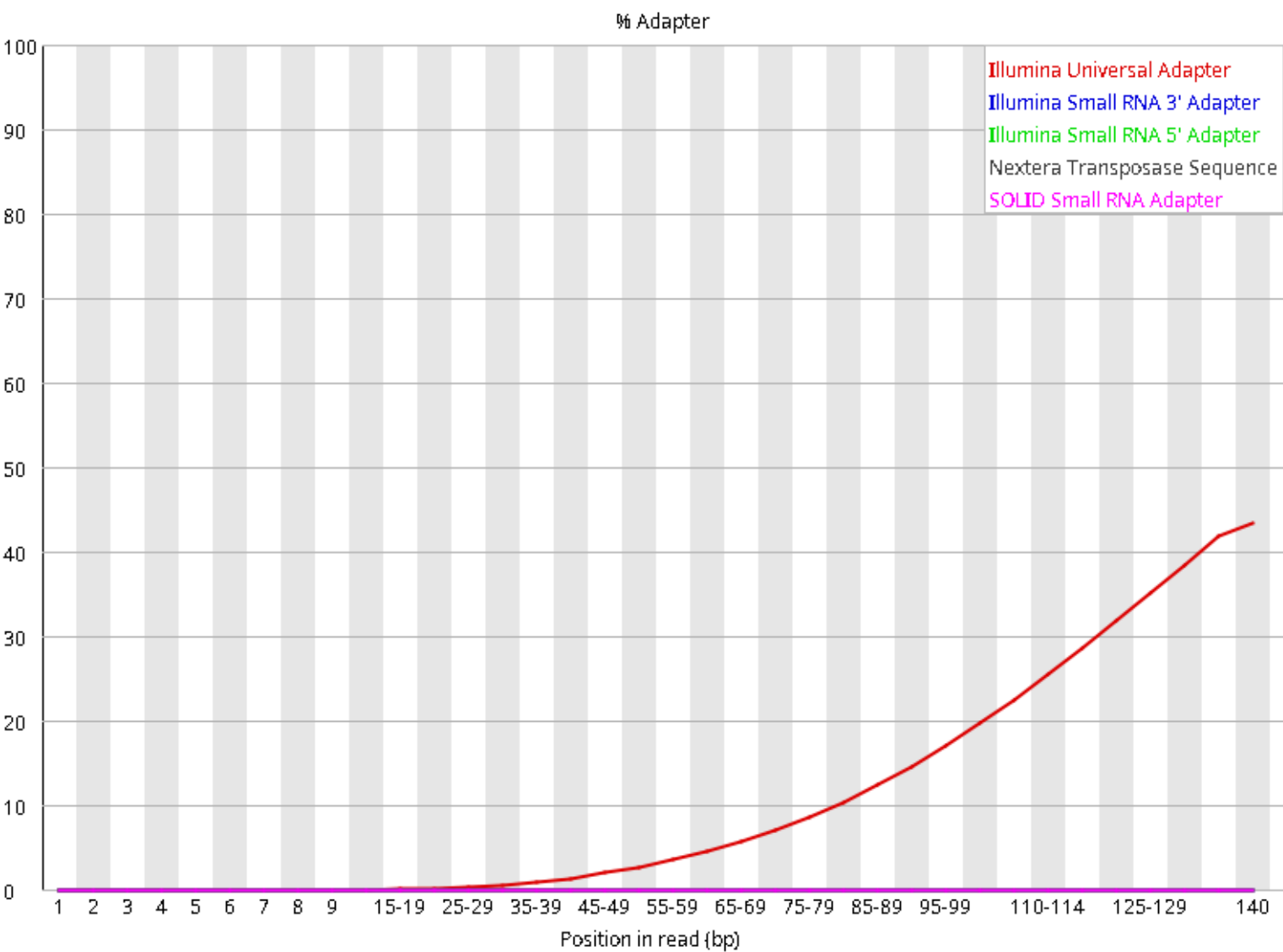


## Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACGCGGTATTATCTCGTAT	1837	1.4954777469329275	TruSeq Adapter, Index 20 (97% over 37bp)
GATCGGAAGAGCACACGTCTGAACTCCAGTCACGCGGTATTATCGCGTAT	295	0.24015565342689907	TruSeq Adapter, Index 20 (97% over 37bp)
CCTCCAATTCCCCCTATCATTTTTGGTTTCCATTTTCCTGGTAAATTTAT	193	0.15711878342844582	No Hit
CCTCCAATTCCTCTATCATTTTTGGTTTCCATTTTCCTGGTAAATTTAT	158	0.1286257398015256	No Hit
CTCCAATTCCCCCTATCATTTTTGGTTTCCATTTTCCTGGTAAATTTATT	125	0.10176087009614367	No Hit



## Adapter Content



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